GeneListSignificanceViewer Documentation

Module name: GeneListSignificanceViewer
Description: File viewer suitable for viewing the results
from marker analysis
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Release: 1.1

Summary: This is a tool that allows the user to view the gene lists produced by the gene neighbor analysis tools ClassNeighbors and GeneNeighbors. For viewing the results of ClassNeighbors, the viewer includes an interactive plot of the permuted scores. Toggle between the views of the markers of each class by selecting the appropriate menu item in the Window menu. When viewing the results of GeneNeighbors, the viewer includes an interactive plot of the distance to the reference gene vs. the gene rank.

The following additional features applies to viewing the results from both ClassNeighbors and GeneNeighbors. Clicking on a point in the plot selects the corresponding element in the table and selecting an element in the table highlights the corresponding data point in the plot. Users can zoom in and out of the plot by clicking and dragging the mouse or by selecting View -> Zoom In or View -> Zoom Out. The scale of the plot can be reset to its original value by choosing the Reset menu item in the View menu. Elements in the table can be selected individually with the mouse. To select all table elements choose Edit -> Select All. Users can search for features by selecting Edit -> Find. Selected table elements can be copied by picking Edit -> Copy. Selecting File -> Save Image will save an image of the plot and selecting File -> Print will print the plot. To retrieve information about Affymetrix probe ids using GeneCruiser, choose the Select Annotations item under the GeneCruiser menu. Select the features you want to retrieve annotations for in the table. Next choose what fields to retrieve from GeneCruiser in the GeneCruiser dialog. Annotations will appear in additional columns in the table.

References:

- none

Parameters:

Name	Description
inputfilename:	odf format file from marker analysis

Return Value: An R list with components:

1. Stdout: the "stdout" text output from running the program.
2. Stderr: the "stderr" error report from running the program.

Platform dependencies:

Task type: Visualizer

CPU type: any
OS: any
Java JVM level: 1.3
Language: Java
Support files: none

Native command line: <java> <java_flags> -cp
<libdir>plot.jar<path.separator><libdir>jai_core.jar<path.separator><libdir>jai_codec.jar<path.
separator><libdir>Jama-1.0.1.jar<path.separator><libdir>MAGEstk-2003-10-24-v1.1-
compatible.jar<path.separator><libdir>broad-cg.jar<path.separator><libdir>jakarta-oro-
2.0.8.jar<path.separator><libdir>trove.jar<path.separator><libdir>GeneListSignificanceViewer
.jar edu.mit.broad.modules.genelist.Viewer <inputfilename>